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RAW SEQUENCE LISTING   DATE: 08/15/2001
PATENT APPLICATION: US/09/486,882   TIME: 09:29:27

Input Set : A:\Try22410.app
Output Set: N:\CRF3\08132001\I486882.raw

ENTERED

p.5

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       3 <110> APPLICANT: Rowett Research Institute Services limited
       5 <120> TITLE OF INVENTION: Chimeric binding peptide library screening method
       7 <130> FILE REFERENCE: P22410-/scr/bou
C-->   9 <140> CURRENT APPLICATION NUMBER: US/09/486,882
C-->  10 <141> CURRENT FILING DATE: 2000-03-02
      12 <160> NUMBER OF SEQ ID NOS: 78
      14 <170> SOFTWARE: PatentIn Ver. 2.0
      16 <210> SEQ ID NO: 1
      17 <211> LENGTH: 521
      18 <212> TYPE: DNA
      19 <213> ORGANISM: Recombinant human oestrogen
      21 <220> FEATURE:
      22 <221> NAME/KEY: CDS
      23 <222> LOCATION: (41)..(475)
      25 <400> SEQUENCE: 1
      26 aagcttgcat gcaaattcta tttcaaggag acagtcataa atg aaa tac cta ttg    55
      27                                                 Met Lys Tyr Leu Leu
      28                                                 1               5
      30 cct acg gca gcc gct gga ttg tta tta ctc gcg gcc cag ccg gcc atg   103
      31 Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala Ala Gln Pro Ala Met
      32               10                    15                  20
      34 gcc caa gtg cag ctg cag taa tag gcg gcc gca ggg gga gga ggg tcc   151
      35 Ala Gln Val Gln Leu Gln         Ala Ala Ala Gly Gly Gly Gly Ser
W-->  36               25               30                  35
      38 atg gaa tct gcc aag gag act cgc tac tgt gca gtg tgc aat gac tat   199
      39 Met Glu Ser Ala Lys Glu Thr Arg Tyr Cys Ala Val Cys Asn Asp Tyr
W-->  40           40              45              50
      42 gct tca ggc tac cat tat gga gtc tgg tcc tgt gag ggc tgc aag gcc   247
      43 Ala Ser Gly Tyr His Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala
W-->  44           55              60              65
      46 ttc ttc aag aga agt att caa gga cat aac gac tat atg tgt cca gcc   295
      47 Phe Phe Lys Arg Ser Ile Gln Gly His Asn Asp Tyr Met Cys Pro Ala
W-->  48 70                  75              80                  85
      50 acc aac cag tgc acc att gat aaa aac agg agg aag agc tgc cag gcc   343
      51 Thr Asn Gln Cys Thr Ile Asp Lys Asn Arg Arg Lys Ser Cys Gln Ala
W-->  52               90              95              100
      54 tgc cgg ctc cgt aaa tgc tac gaa gtg gga atg atg aaa ggt ggg ata   391
      55 Cys Arg Leu Arg Lys Cys Tyr Glu Val Gly Met Met Lys Gly Gly Ile
W-->  56           105             110                 115
      58 cga aaa gac cga aga gga ggg aga atg ttg aaa cac aag cgc cag aga   439
      59 Arg Lys Asp Arg Arg Gly Gly Arg Met Leu Lys His Lys Arg Gln Arg
W-->  60           120             125                 130
      62 gat gat ggg gag ggc agg ggt gaa gtg ggg tct tga taatcaggtc        485
      63 Asp Asp Gly Glu Gly Arg Gly Glu Val Gly Ser
W-->  64           135             140                 145
      66 agagtgacct gagctaaaat aacacattca gaattc                          521
      69 <210> SEQ ID NO: 2
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Input Set : **A:\Try22410.app**
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70 <211> LENGTH: 27
71 <212> TYPE: PRT
72 <213> ORGANISM: Recombinant human oestrogen
74 <400> SEQUENCE: 2
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78 Ala Gln Pro Ala Met Ala Gln Val Gln Leu Gln
79              20                  25
82 <210> SEQ ID NO: 3
83 <211> LENGTH: 115
84 <212> TYPE: PRT
85 <213> ORGANISM: Recombinant human oestrogen
87 <400> SEQUENCE: 3
88 Ala Ala Ala Gly Gly Gly Gly Ser Met Glu Ser Ala Lys Glu Thr Arg
89   1               5                  10                  15
91 Tyr Cys Ala Val Cys Asn Asp Tyr Ala Ser Gly Tyr His Tyr Gly Val
92              20                  25                  30
94 Trp Ser Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser Ile Gln Gly
95              35                  40                  45
97 His Asn Asp Tyr Met Cys Pro Ala Thr Asn Gln Cys Thr Ile Asp Lys
98         50                  55                  60
100 Asn Arg Arg Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys Cys Tyr Glu
101  65                  70                  75                  80
103 Val Gly Met Met Lys Gly Gly Ile Arg Lys Asp Arg Arg Gly Gly Arg
104                  85                  90                  95
106 Met Leu Lys His Lys Arg Gln Arg Asp Asp Gly Glu Gly Arg Gly Glu
107                 100                 105                 110
109 Val Gly Ser
110         115
113 <210> SEQ ID NO: 4
114 <211> LENGTH: 102
115 <212> TYPE: DNA
116 <213> ORGANISM: human
118 <220> FEATURE:
119 <221> NAME/KEY: CDS
120 <222> LOCATION: (1)..(102)
122 <400> SEQUENCE: 4
123 aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat   48
124 Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
125   1               5                  10                  15
127 gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac   96
128 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
129              20                  25                  30
131 ttc tat                                                          102
132 Phe Tyr
135 <210> SEQ ID NO: 5
136 <211> LENGTH: 34
137 <212> TYPE: PRT
138 <213> ORGANISM: human
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140 <400> SEQUENCE: 5
141 Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
142   1               5                   10                  15
144 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
145               20                  25                  30
147 Phe Tyr
151 <210> SEQ ID NO: 6
152 <211> LENGTH: 150
153 <212> TYPE: DNA
154 <213> ORGANISM: Human lymphocyte
156 <220> FEATURE:
157 <221> NAME/KEY: CDS
158 <222> LOCATION: (1)..(150)
160 <220> FEATURE:
162 <400> SEQUENCE: 6
163 atg gcc cag ccc acc acg cgt ccg ggc caa ggg aca cga ctg gac att      48
164 Met Ala Gln Pro Thr Thr Arg Pro Gly Gln Gly Thr Arg Leu Asp Ile
165   1               5                   10                  15
167 aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat      96
168 Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
169               20                  25                  30
171 gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac     144
172 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
173               35                  40          ,       45
175 ttc tat                                                             150
176 Phe Tyr
177       50
180 <210> SEQ ID NO: 7
181 <211> LENGTH: 50
182 <212> TYPE: PRT
183 <213> ORGANISM: Human lymphocyte
185 <400> SEQUENCE: 7
186 Met Ala Gln Pro Thr Thr Arg Pro Gly Gln Gly Thr Arg Leu Asp Ile
187   1               5                   10                  15
189 Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
190               20                  25                  30
192 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
193               35                  40                  45
195 Phe Tyr
196       50
199 <210> SEQ ID NO: 8
200 <211> LENGTH: 150
201 <212> TYPE: DNA
202 <213> ORGANISM: Human lymphocyte
204 <220> FEATURE:
205 <221> NAME/KEY: CDS
206 <222> LOCATION: (1)..(150)
208 <400> SEQUENCE: 8
209 atg gcc cag tcc cac cac gcg tcc ggc gga ggg acc aag gtg gag atc      48
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211   1               5                 10                  15
213 aaa cga act gtg gct gca cca tct gtc ttc atc ttc ccg cca tct gat   96
214 Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
215               20                  25                  30
217 gag cag ttg aaa tct gga act gcc tct gtt gtg tgc ctg ctg aat aac  144
218 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
219           35                  40                  45
221 ttc tat                                                          150
222 Phe Tyr
223     50
226 <210> SEQ ID NO: 9
227 <211> LENGTH: 50
228 <212> TYPE: PRT
229 <213> ORGANISM: Human lymphocyte
231 <400> SEQUENCE: 9
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233   1               5                 10                  15
235 Lys Arg Thr Val Ala Ala Pro Ser Val Phe Ile Phe Pro Pro Ser Asp
236               20                  25                  30
238 Glu Gln Leu Lys Ser Gly Thr Ala Ser Val Val Cys Leu Leu Asn Asn
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241 Phe Tyr
242     50
245 <210> SEQ ID NO: 10
246 <211> LENGTH: 566
247 <212> TYPE: DNA
248 <213> ORGANISM: Recombinant human oestrogen
250 <220> FEATURE:
251 <221> NAME/KEY: CDS
252 <222> LOCATION: (41)..(475)
254 <400> SEQUENCE: 10
255 aagcttgcat gcaaattcta tttcaaggag acagtcataa atg aaa tac cta ttg   55
256                                             Met Lys Tyr Leu Leu
257                                               1               5
259 cct acg gca gcc gct gga ttg tta tta ctc gcg gcc cag ccg gcc atg  103
260 Pro Thr Ala Ala Ala Gly Leu Leu Leu Leu Ala Ala Gln Pro Ala Met
261                   10              15                  20
263 gcc gag gtg caa ctg cag taa tag gcg gcc gca ggg gga gga ggg tcc  151
264 Ala Glu Val Gln Leu Gln         Ala Ala Ala Gly Gly Gly Gly Ser
W--> 265           25                  30                  35
267 atg gaa tct gcc aag gag act cgc tac tgt gca gtg tgc aat gac tat  199
268 Met Glu Ser Ala Lys Glu Thr Arg Tyr Cys Ala Val Cys Asn Asp Tyr
W--> 269           40                  45                  50
271 gct tca ggc tac cat tat gga gtc tgg tcc tgt gag ggc tgc aag gcc  247
272 Ala Ser Gly Tyr His Tyr Gly Val Trp Ser Cys Glu Gly Cys Lys Ala
W--> 273     55                  60                  65
275 ttc ttc aag aga agt att caa gga cat aac gac tat atg tgt cca gcc  295
276 Phe Phe Lys Arg Ser Ile Gln Gly His Asn Asp Tyr Met Cys Pro Ala
```

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```
W--> 277  70                 75                80                85
    279 acc aac cag tgc acc att gat aaa aac agg agg aag agc tgc cag gcc  343
    280 Thr Asn Gln Cys Thr Ile Asp Lys Asn Arg Arg Lys Ser Cys Gln Ala
W--> 281                 90                95               100
    283 tgc cgg ctc cgt aaa tgc tac gaa gtg gga atg atg aaa ggt ggg ata  391
    284 Cys Arg Leu Arg Lys Cys Tyr Glu Val Gly Met Met Lys Gly Gly Ile
W--> 285            105               110               115
    287 cga aaa gac cga aga gga ggg aga atg ttg aaa cac aag cgc cag aga  439
    288 Arg Lys Asp Arg Arg Gly Gly Arg Met Leu Lys His Lys Arg Gln Arg
W--> 289         120              125              130
    291 gat gat ggg gag ggc agg ggt gaa gtg ggg tct tga taatcaggtc  485
    292 Asp Asp Gly Glu Gly Arg Gly Glu Val Gly Ser
W--> 293     135              140              145
    295 agagtgacct gagctaaaat aacacattca ggtcgacttg ggtcagtctg accgggacaa  545
    297 agttaatgta acctcgaatt c                                           566
    300 <210> SEQ ID NO: 11
    301 <211> LENGTH: 27
    302 <212> TYPE: PRT
    303 <213> ORGANISM: Recombinant human oestrogen
    305 <400> SEQUENCE: 11
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    307 1               5                  10                  15
    309 Ala Gln Pro Ala Met Ala Glu Val Gln Leu Gln
    310             20                  25
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    314 <211> LENGTH: 115
    315 <212> TYPE: PRT
    316 <213> ORGANISM: Recombinant human oestrogen
    318 <400> SEQUENCE: 12
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    320 1               5                  10                  15
    322 Tyr Cys Ala Val Cys Asn Asp Tyr Ala Ser Gly Tyr His Tyr Gly Val
    323             20                  25                  30
    325 Trp Ser Cys Glu Gly Cys Lys Ala Phe Phe Lys Arg Ser Ile Gln Gly
    326         35                  40                  45
    328 His Asn Asp Tyr Met Cys Pro Ala Thr Asn Gln Cys Thr Ile Asp Lys
    329     50                  55                  60
    331 Asn Arg Arg Lys Ser Cys Gln Ala Cys Arg Leu Arg Lys Cys Tyr Glu
    332 65                  70                  75                  80
    334 Val Gly Met Met Lys Gly Gly Ile Arg Lys Asp Arg Arg Gly Gly Arg
    335             85                  90                  95
    337 Met Leu Lys His Lys Arg Gln Arg Asp Asp Gly Glu Gly Arg Gly Glu
    338             100                 105               110
    340 Val Gly Ser
    341         115
    344 <210> SEQ ID NO: 13
    345 <211> LENGTH: 539
    346 <212> TYPE: DNA
    347 <213> ORGANISM: Recombinant human oestrogen
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Please Note:
Use of n and/or Xaa have been detected in the Sequence Listing. Please review the
Sequence Listing to ensure that a corresponding explanation is presented in the <220> to
<223> fields of each sequence which presents at least one n or Xaa.

VERIFICATION SUMMARY. •   DATE: 08/15/2001
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Input Set : **A:\Try22410.app**
Output Set: **N:\CRF3\08132001\I486882.raw**

```
L:9 M:270 C: Current Application Number differs, Replaced Current Application Number
L:10 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:36 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:40 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:44 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:48 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:52 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:56 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:60 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:64 M:336 W: Invalid Amino Acid Number in Coding Region, SEQ ID:1
L:265 M:336 W:  Invalid Amino Acid Number in Coding Region, SEQ ID:10
L:269 M:336 W:  Invalid Amino Acid Number in Coding Region, SEQ ID:10
L:273 M:336 W:  Invalid Amino Acid Number in Coding Region, SEQ ID:10
L:277 M:336 W:  Invalid Amino Acid Number in Coding Region, SEQ ID:10
L:281 M:336 W:  Invalid Amino Acid Number in Coding Region, SEQ ID:10
L:285 M:336 W:  Invalid Amino Acid Number in Coding Region, SEQ ID:10
L:289 M:336 W:  Invalid Amino Acid Number in Coding Region, SEQ ID:10
L:293 M:336 W:  Invalid Amino Acid Number in Coding Region, SEQ ID:10
L:612 M:258 W: Mandatory Feature missing, <221> not found for SEQ ID#:21
L:612 M:258 W: Mandatory Feature missing, <222> not found for SEQ ID#:21
L:612 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:21
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